



387	GAG AAA CTG TTG CAG TGA AGC CAA CAG AAA ACA ATG AAG AGG AAT TCA CCT CAA	396		405	414	423	432
				M K R N S P Q			
441	AAG ATA AAA AGA AAG GAC AGA AGG GCA AAA AAA CAG AGT TTTT GAT GAT AAT	450	459	468	477	486	
K I K K R K D R R A K Q S F D N							
495	GAT AGC GAA GAA TTG GAA GAT AAA GAT TCA AAA AAG ACT GCA AAA CCG	504	513	522	531	540	
D S E E L E D K D S K K T A K P							
549	AAA GTG GAA ATG TAC TCT GGG AGT GAT GAT GAT TTT AAC AAA CTT CCT	558	567	576	585	594	
K V E M Y S S G S D D D F N K L P							
603	AAA AAA GCT AAA GGG AAA GCT CAA AAA TCA AAT AAG AAG TGG GAT GGG TCA GAG	612	621	630	639	648	
K K A K G K A Q K S N K K W D G S E							
657	GAG GAT GAG AAC AGT AAA AGA ATT AAA GAG CGT TCA AGA ATA AAT TCT TCT	666	675	684	693	702	
E D E D N S S K K I K E R S R I N S S							
711	GGT GAA AGT GGT GAT GAA TCA GAT GAA TTT TTG CAA TCT AGA AAA GGA CAG AAA	720	729	738	747	756	
G E S G D E S S D E F L Q S R K G Q K							

FIGURE 1B

765	774	783	792	801	810
AAA AAT CAG AAA AAC AAG CCA GGT CCT AAC ATA GAA AGT GGG AAT GAA GAT GAT					
K N Q K N K P G P N I E S G N E D D					
819	828	837	846	855	864
GAC GCC TCC TTC AAA ATT AAG ACA GTG GCC CAA AAG AAG GCA GAA AAG AAG GAG					
D A S F K I K T V A Q K K A E K K E					
873	882	891	900	909	918
CGC GAG AGA AAA AAG CGA GAT GAA GAA AAA GCG AAA CTG CGG AAG CTG AAA GAA					
R E R K K R D E E K A K L R K L K E					
927	936	945	954	963	972
AAA GAA GAG TTA GAA ACA GGT AAA AAG GAT CAG AGT AAA CAA AAG GAA TCT CAA					
K E E L E T G K K D Q S K Q K E S Q					
981	990	999	1008	1017	1026
AGG AAA TTT GAA GAA GAA ACT GTA AAA TCC AAA GTG ACT GTT GAT ACT GGA GTA					
R K F E E E T V K S K V T V D T G V					
1035	1044	1053	1062	1071	1080
ATT CCT GCC TCT GAA GAG AAA GCA GAG ACT CCC ACA GCT GCA GAA GAT GAC AAT					
I P A S E E K A E T P T A A E D D N					
1089	1098	1107	1116	1125	1134
GAA GGA GAC AAA AAG AAG AAA GAT AAG AAG AAA AAG AAA GGA GAA AAG GAA GAA					
E G D K K K K D K K K K K G E K E E					

FIGURE 1C

1143	1152	1161	1170	1179	1188
AAA GAG AAA GAG AAG AAA AAA GGA CCT AGC AAA GCC ACT GTT AAA GCT ATG CAA					
K E K E K K K K G P S K A T V K A M Q					
1197	1206	1215	1224	1233	1242
GAA GCT CTG GCT AAG CTT AAA GAG GAA GAA GAA AGA CAG AAG AGA GAA GAG GAA					
E A L A K L K L K E E E R Q K R E E E					
1251	1260	1269	1278	1287	1296
GAA CGT ATA AAA CGG CTT GAA GAA TTA GAA AGC AAG CCG TAA GCA CAA GGA ACC					
E R I K R L E L E L E S K P					
1305	1314	1323	1332	1341	1350
GTT TGG AAC CCA GAC CAA AAG AGC AAG GGC ACA GGC AAG ACA CCA AAC CAA GGG					
1359	1368	1377	1386	1395	1404
GCG GCC CCC GAA TTA ATG TAC CTC TTC GCA CCG GGA CTT CCT TTC GGG GCC GTT					
1413	1422	1431			
CCT GCA AGC GGA ACC AAT TTT CCC TAA AGG 3'					

FIGURE 1D

1 MKRNSPQKIKKRRKDRRAKKQSFDDNDSEEL EDKDSKSKT NABP-1  
1 - - - - - GQKGGKTSFD ENDS EEL EDKDSKSKP g1514949

41 AKPKVE - MYSGSDDDDFNKKLPKKAKGKAQKSNKKWDGSE NABP-1  
28 ARPNSE VLLSGSEDAADDPNKL SKKGK - KAAQKSTKKRDGSE g1514949

80 EEDNSKKIKERSRINSSGESGDESDEF LQSRKGGQKKNQK NABP-1  
67 EEDNSKRSKERSRVNSSGESGGESEDEF LQSRKGGQKKNQK g1514949

120 NKP GPNIESGNEDDDA SFKIKTV AQKKAEKKERERKKRDE NABP-1  
107 NKSVPITIDSGNEDDDS SFKIKTV AQKKAEKKERERKKRE g1514949

160 EKA KLRKLKEKEEEL ETGKKDQSKQKESQRRKFEETVKS KV NABP-1  
147 EKA KLRKVKEKEEEL EKGRKEQSKQRE PQKRPDEEVLVLRG g1514949

200 TVDTGVIPASEEKAETPTAA EDDN EGDKKKDKKKKGEK NABP-1  
187 TPDAG - - AASEEKGDI AATLEDDN EGDKKKDKKKKT EK g1514949

240 EEKEKEKKGP SKATVKAMQEALAKLKEEEERQKREER NABP-1  
225 DDKEKEKKKG g1514949

280 IKRLEEL ES KP NABP-1  
234 g1514949

FIGURE 2

FIGURE 3A

"CELL" SEQUENCE

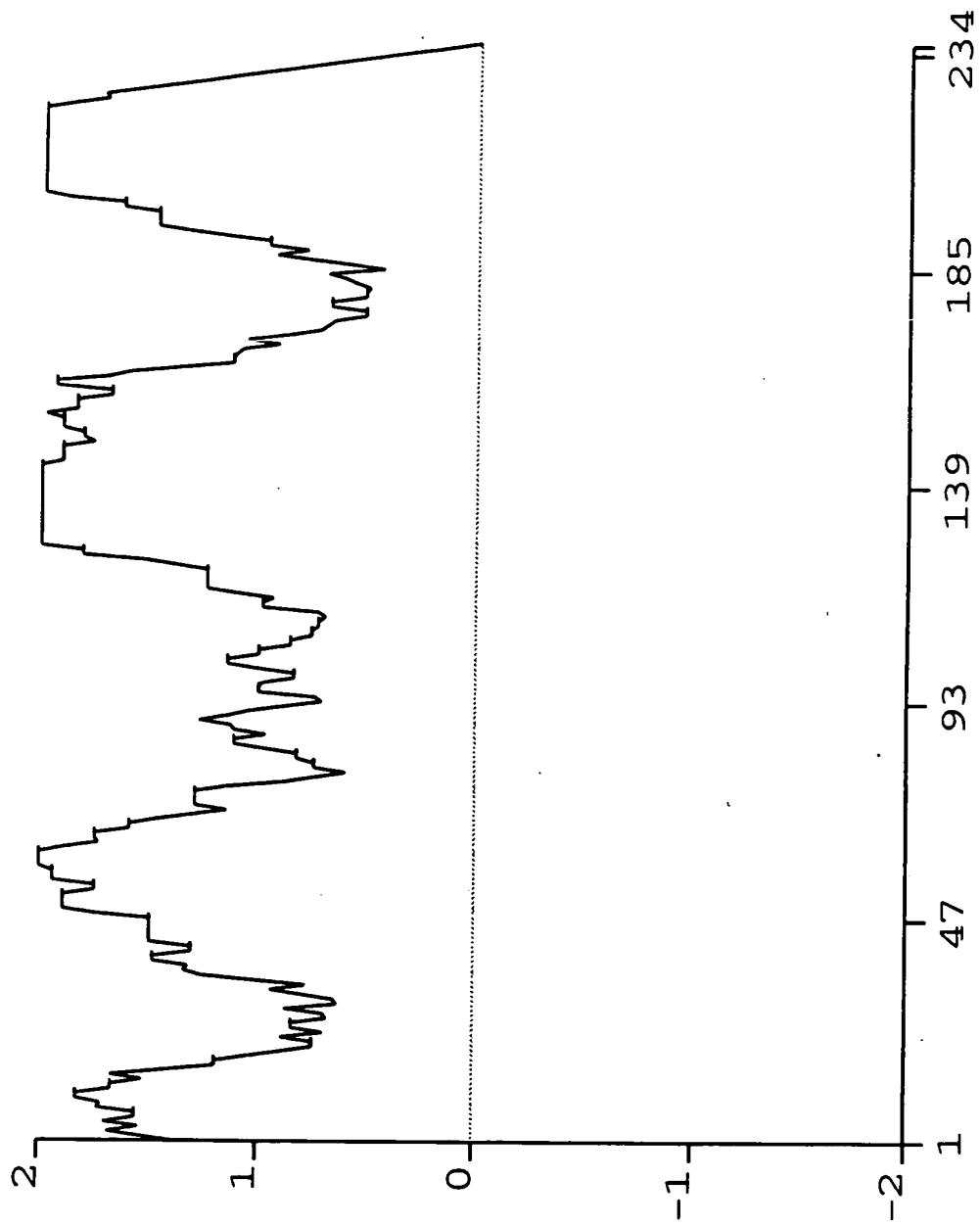


FIGURE 3B